

SEQUENCE LISTING

<110> David M. Knipe
 Travis J. Taylor
 Elizabeth McNamee

<120> Replication-Competent Virus Expressing A
 Fusion Protein

<130> HU98-05

<140> 09/127,227

<141> 1998-07-31

<160> 5

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 4359

<212> DNA

<213> herpesvirus

<220>

<221> CDS

<222> (1)...(4359)

<400> 1

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520

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Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys		

1365

1370

1375

gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag ctg 4176
 Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 1380 1385 1390

gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg ctc 4224
 Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 1395 1400 1405

ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa gat 4272
 Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp
 1410 1415 1420

ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc gct 4320
 Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
 1425 1430 1435 1440

gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 4359
 Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys *
 1445 1450

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<400> 2

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 Pro Leu Gly Tyr Val Tyr Ala Arg Ala Cys Pro Ser Glu Gly Ile Glu
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 Leu Leu Ala Leu Leu Ser Ala Arg Ser Gly Asp Ala Asp Val Ala Val
 35 40 45
 Ala Pro Leu Val Val Gly Leu Thr Val Glu Ser Gly Phe Glu Ala Asn
 50 55 60
 Val Ala Val Val Val Gly Ser Arg Thr Thr Gly Leu Gly Gly Thr Ala
 65 70 75 80
 Val Ser Leu Lys Leu Thr Pro Ser His Tyr Ser Ser Ser Val Tyr Val
 85 90 95
 Phe His Gly Gly Arg His Leu Asp Pro Ser Thr Gln Ala Pro Asn Leu
 100 105 110
 Thr Arg Leu Cys Glu Arg Ala Arg Arg His Phe Gly Phe Ser Asp Tyr
 115 120 125
 Thr Pro Arg Pro Gly Asp Leu Lys His Glu Thr Thr Gly Glu Ala Leu
 130 135 140
 Cys Glu Arg Leu Gly Leu Asp Pro Asp Arg Ala Leu Leu Tyr Leu Val
 145 150 155 160
 Val Thr Glu Gly Phe Lys Glu Ala Val Cys Ile Asn Asn Thr Phe Leu
 165 170 175
 His Leu Gly Gly Ser Asp Lys Val Thr Ile Gly Gly Ala Glu Val His
 180 185 190

Arg	Ile	Pro	Val	Tyr	Pro	Leu	Gln	Leu	Phe	Met	Pro	Asp	Phe	Ser	Arg
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Val	Ile	Ala	Glu	Pro	Phe	Asn	Ala	Asn	His	Arg	Ser	Ile	Gly	Glu	Asn
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Phe	Thr	Tyr	Pro	Leu	Pro	Phe	Phe	Asn	Arg	Pro	Leu	Asn	Arg	Leu	Leu
225					230					235					240
Phe	Glu	Ala	Val	Val	Gly	Pro	Ala	Ala	Val	Ala	Leu	Arg	Cys	Arg	Asn
			245						250					255	
Val	Asp	Ala	Val	Ala	Arg	Ala	Ala	Ala	His	Leu	Ala	Phe	Asp	Glu	Asn
			260					265					270		
His	Glu	Gly	Ala	Ala	Leu	Pro	Ala	Asp	Ile	Thr	Phe	Thr	Ala	Phe	Glu
		275					280					285			
Ala	Ser	Gln	Gly	Lys	Thr	Pro	Arg	Gly	Gly	Arg	Asp	Gly	Gly	Gly	Lys
	290					295					300				
Gly	Pro	Ala	Gly	Gly	Phe	Glu	Gln	Arg	Leu	Ala	Ser	Val	Met	Ala	Gly
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Asp	Ala	Ala	Leu	Ala	Leu	Glu	Ser	Ile	Val	Ser	Met	Ala	Val	Phe	Asp
				325					330					335	
Glu	Pro	Pro	Thr	Asp	Ile	Ser	Ala	Trp	Pro	Leu	Cys	Glu	Gly	Gln	Asp
			340					345					350		
Thr	Ala	Ala	Ala	Arg	Ala	Asn	Ala	Val	Gly	Ala	Tyr	Leu	Ala	Arg	Ala
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Ala	Gly	Leu	Val	Gly	Ala	Met	Val	Phe	Ser	Thr	Asn	Ser	Ala	Leu	His
	370					375					380				
Leu	Thr	Glu	Val	Asp	Asp	Ala	Gly	Pro	Ala	Asp	Pro	Lys	Asp	His	Ser
385					390					395					400
Lys	Pro	Ser	Phe	Tyr	Arg	Phe	Phe	Leu	Val	Pro	Gly	Thr	His	Val	Ala
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Ala	Asn	Pro	Gln	Val	Asp	Arg	Glu	Gly	His	Val	Val	Pro	Gly	Phe	Glu
			420					425					430		
Gly	Arg	Pro	Thr	Ala	Pro	Leu	Val	Gly	Gly	Thr	Gln	Glu	Phe	Ala	Gly
		435					440					445			
Glu	His	Leu	Ala	Met	Leu	Cys	Gly	Phe	Ser	Pro	Ala	Leu	Leu	Ala	Lys
	450					455					460				
Met	Leu	Phe	Tyr	Leu	Glu	Arg	Cys	Asp	Gly	Gly	Val	Ile	Val	Gly	Arg
465					470					475					480
Gln	Glu	Met	Asp	Val	Phe	Arg	Tyr	Val	Ala	Asp	Ser	Asn	Gln	Thr	Asp
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Val	Pro	Cys	Asn	Leu	Cys	Thr	Phe	Asp	Thr	Arg	His	Ala	Cys	Val	His
			500					505					510		
Thr	Thr	Leu	Met	Arg	Leu	Arg	Ala	Arg	His	Pro	Lys	Phe	Ala	Ser	Ala
		515					520					525			
Ala	Arg	Gly	Ala	Ile	Gly	Val	Phe	Gly	Thr	Met	Asn	Ser	Met	Tyr	Ser
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Asp	Cys	Asp	Val	Leu	Gly	Asn	Tyr	Ala	Ala	Phe	Ser	Ala	Leu	Lys	Arg
545					550					555					560
Ala	Asp	Gly	Ser	Glu	Thr	Ala	Arg	Thr	Ile	Met	Gln	Glu	Thr	Tyr	Arg
			565						570					575	
Ala	Ala	Thr	Glu	Arg	Val	Met	Ala	Glu	Leu	Glu	Thr	Leu	Gln	Tyr	Val
		580						585					590		
Asp	Gln	Ala	Val	Pro	Thr	Ala	Met	Gly	Arg	Leu	Glu	Thr	Ile	Ile	Thr
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Asn	Arg	Glu	Ala	Leu	His	Thr	Val	Val	Asn	Asn	Val	Arg	Gln	Val	Val

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Asp	Arg	Glu	Val	Glu	Gln	Leu	Met	Arg	Asn	Leu	Val	Glu	Gly	Arg	Asn
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Phe	Lys	Phe	Arg	Asp	Gly	Leu	Gly	Glu	Ala	Asn	His	Ala	Met	Ser	Leu
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Thr	Leu	Asp	Pro	Tyr	Ala	Cys	Gly	Pro	Cys	Pro	Leu	Leu	Gln	Leu	Leu
			660					665					670		
Gly	Arg	Arg	Ser	Asn	Leu	Ala	Val	Tyr	Gln	Asp	Leu	Ala	Leu	Ser	Gln
		675					680					685			
Cys	His	Gly	Val	Phe	Ala	Gly	Gln	Ser	Val	Glu	Gly	Arg	Asn	Phe	Arg
	690					695					700				
Asn	Gln	Phe	Gln	Pro	Val	Leu	Arg	Arg	Arg	Val	Met	Asp	Met	Phe	Asn
705					710						715				720
Asn	Gly	Phe	Leu	Ser	Ala	Lys	Thr	Leu	Thr	Val	Ala	Leu	Ser	Glu	Gly
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Ala	Ala	Ile	Cys	Ala	Pro	Ser	Leu	Thr	Ala	Gly	Gln	Thr	Ala	Pro	Ala
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Lys	Glu	Leu	Arg	Val	Lys	Ser	Arg	Val	Leu	Phe	Ala	Gly	Ala	Ser	Ala
	770					775						780			
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785					790					795					800
Tyr	Gln	Lys	Pro	Asp	Lys	Arg	Val	Asp	Ile	Leu	Leu	Gly	Pro	Leu	Gly
				805					810					815	
Phe	Leu	Leu	Lys	Gln	Phe	His	Ala	Ala	Ile	Phe	Pro	Asn	Gly	Lys	Pro
			820					825					830		
Pro	Gly	Ser	Asn	Gln	Pro	Asn	Pro	Gln	Trp	Phe	Trp	Thr	Ala	Leu	Gln
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	850					855					860				
Ile	Ala	Phe	Ile	Lys	Lys	Phe	Ser	Leu	Asp	Tyr	Gly	Ala	Ile	Asn	Phe
865					870					875				880	
Ile	Asn	Leu	Ala	Pro	Asn	Asn	Val	Ser	Glu	Leu	Ala	Met	Tyr	Tyr	Met
				885					890					895	
Ala	Asn	Gln	Ile	Leu	Arg	Tyr	Cys	Asp	His	Ser	Thr	Tyr	Phe	Ile	Asn
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Thr	Leu	Thr	Ala	Ile	Ile	Ala	Gly	Ser	Arg	Arg	Pro	Pro	Ser	Val	Gln
		915					920					925			
Ala	Ala	Ala	Ala	Trp	Ser	Ala	Gln	Gly	Gly	Ala	Gly	Leu	Glu	Ala	Gly
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Ala	Arg	Ala	Leu	Met	Asp	Ala	Val	Asp	Ala	His	Pro	Gly	Ala	Trp	Thr
945					950					955				960	
Ser	Met	Phe	Ala	Ser	Cys	Asn									

Gly	Gly	Gly	Ala	His	Glu	Ser	Ser	Leu	Cys	Glu	Gln	Leu	Arg	Gly	Ile	
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Ile	Ser	Glu	Gly	Gly	Ala	Ala	Val	Ala	Ser	Ser	Val	Phe	Val	Ala	Thr	
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Val	Lys	Ser	Leu	Gly	Pro	Arg	Thr	Gln	Gln	Leu	Gln	Ile	Glu	Asp	Trp	
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Leu	Ala	Leu	Leu	Glu	Asp	Glu	Tyr	Leu	Ser	Glu	Glu	Met	Met	Glu	Leu	
	1090					1095					1100					
Thr	Ala	Arg	Ala	Leu	Glu	Arg	Gly	Asn	Gly	Glu	Trp	Ser	Thr	Asp	Ala	
1105					1110					1115					1120	
Ala	Leu	Glu	Val	Ala	His	Glu	Ala	Glu	Ala	Leu	Val	Ser	Gln	Leu	Gly	
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Asn	Ala	Gly	Glu	Val	Phe	Asn	Phe	Gly	Asp	Phe	Gly	Cys	Glu	Asp	Asp	
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Asn	Ala	Thr	Pro	Phe	Gly	Gly	Pro	Gly	Ala	Pro	Gly	Pro	Ala	Phe	Ala	
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Gly	Arg	Lys	Arg	Ala	Phe	His	Gly	Asp	Asp	Pro	Phe	Gly	Glu	Gly	Pro	
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Pro	Asp	Lys	Lys	Gly	Asp	Leu	Thr	Leu	Asp	Met	Leu	Arg	Gly	Val	Gly	
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Gly	Trp	Gly	Asn	Leu	Glu	Ser	Thr	Arg	Ala	Ala	Ala	Ala	Thr	Met	Ser	
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Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	
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Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	
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Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	
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Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Thr	Tyr	
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Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	
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Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	
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Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	
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Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	
1345					1350					1355					1360	
Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> a sense molecule used to modify the stop codon

<400> 3
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24

<210> 4
 <211> 24
 <212> DNA
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<220>
 <223> an anti-sense molecule used to modify the stop
 codon

<400> 4
 cgttgatg gctgagaggg gttg

24

<210> 5
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide linker

<400> 5
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12